# Steven M. Foltz

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## Education

**PhD, Washington University in St. Louis, St. Louis, MO**  June 2014 – present
Division of Biology and Biomedical Sciences (DBBS)  Expected defense: Winter 2019
Human and Statistical Genetics Program
Precision Medicine Pathway
*Advisor*: Li Ding, PhD
*Thesis*: Multi-platform genomics and transcriptomics integration for gene fusion discovery and somatic mutation haplotyping in cancer

**MS Biostatistics, University of Washington, Seattle, WA**  September 2011 – August 2013
*Advisors*: Brian Browning, PhD, and Sharon Browning, PhD
*Thesis*: Rare variant method for identity-by-descent detection in sequence data, and the time to most recent common ancestor given identity-by-descent segment length

**BS Mathematics, Presbyterian College, Clinton, SC**  August 2006 – April 2010
*Advsor*: Doug Daniel, PhD
*Thesis*: Tiling 2-deficient Rectangles with Trominoes

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## Research Experience

**Washington University in St. Louis, St. Louis, MO**  June 2014 – present
*Graduate student*, Laboratory of Li Ding, PhD
*Thesis*: Multi-platform genomics and transcriptomics integration for gene fusion discovery and somatic mutation haplotyping in cancer

- Pan-cancer computational projects utilizing tumor and normal tissue sequencing data (DNA, RNA to understand multiple types of germline and somatic variation

- Large-scale, integrative data analysis tool and pipeline development, including variant calling and quality control using bulk DNA and RNA, single cell RNA, and linked-read DNA sequencing

- Gene fusion discovery in 9,000+ patients from The Cancer Genome Atlas and a large multiple myeloma cohort

- Linked-read whole genome sequencing data analysis for phasing somatic variation and modeling tumor evolution

My work has led to two first author papers published in *Bioinformatics* and *Cell Reports*, one paper under review, and one in preparation. Additionally, I am co-author on four papers in *Cell*, *Nature Medicine*, *Molecular Psychiatry*, and *Annals of Oncology*.

**Virginia Commonwealth University, Richmond, VA**                    August 2013 – May 2014
*Biostatistician*, Laboratory of Nengliang Yao, PhD

- Led statistical aspects of cancer care research as part of a healthcare policy team

- Procured, cleaned, and analyzed data from national cancer databases, including SEER

- Developed geographically weighted regression and spatial panel data models

This work led to a co-author publication in *PLoS ONE*.

**University of Washington, Seattle, WA**                    September 2011 – August 2013
*Research assistant*, Laboratory of Brian Browning, PhD, and Sharon Browning, PhD
*Thesis*: Rare variant method for identity-by-descent detection in sequence data, and the time to most recent common ancestor given identity-by-descent segment length

- Implemented novel algorithms to define identity-by-descent (IBD) between individuals using rare DNA variation and developed statistical models for shared ancestor inference

- Worked with data from the 1000 Genomes Project and simulated coalescent model data

- Assisted in methods development for missing data imputation and haplotype phasing

**Presbyterian College, Clinton, SC**                    Spring 2010
*Honors research in mathematics*, advised by Doug Daniel, PhD
*Thesis*: Tiling 2-deficient Rectangles with Trominoes

- Developed analytical and computational approaches to answer an open question about tiling deficient rectangular fields with trominos.

**Medical University of South Carolina, Charleston, SC**                    Summer 2009
*Summer Research Fellow*, Laboratory of Jim Zheng, PhD

- Created a weighted clustering coefficient to detect regions of high interconnectivity in yeast gene networks based on synthetic lethal interactions.

**Presbyterian College, Clinton, SC**                    Fall 2008 – Spring 2009
*Research assistant*, Laboratory of James Wanliss, PhD

- Analyzed space weather data as part of a programming team to refine solar storm prediction models.

## Research Grants

**Paula C. and Rodger O. Riney Blood Cancer Research Initiative Fund**
Washington University School of Medicine
Funding since Fall 2017: $25 million
Principal Investigators include: Li Ding, PhD
My contributions:

- Multiple myeloma gene fusion discovery project, single cell RNA analysis, and linked-read whole genome sequencing analysis

- Preparation and delivery of multiple donor presentations

## Publications

1. Sanchez-Vega, F., M. Mina, J. Armenia, W. K. Chatila, A. Luna, K. C. La, S. Dimitriadoy, D. L. Liu, H. S. Kantheti, S. Saghafinia, D. Chakravarty, F. Daian, Q. Gao, M. H. Bailey, W. W. Liang, **S. M. Foltz**, I. Shmulevich, L. Ding, Z. Heins, A. Ochoa, B. Gross, J. Gao, H. Zhang, R. Kundra, C. Kandoth, I. Bahceci, L. Dervishi, U. Dogrusoz, W. Zhou, H. Shen, P. W. Laird, G. P. Way, C. S. Greene, H. Liang, Y. Xiao, C. Wang, A. Iavarone, A. H. Berger, T. G. Bivona, A. J. Lazar, G. D. Hammer, T. Giordano, L. N. Kwong, G. McArthur, C. Huang, A. D. Tward, M. J. Frederick, F. McCormick, M. Meyerson, N. Cancer Genome Atlas Research, E. M. Van Allen, A. D. Cherniack, G. Ciriello, C. Sander and N. Schultz (2018). "Oncogenic Signaling Pathways in The Cancer Genome Atlas." *Cell* **173**(2): 321-337 e310.

2. Gao, Q.*, W. W. Liang*, **S. M. Foltz**\*, G. Mutharasu, R. G. Jayasinghe, S. Cao, W. W. Liao, S. M. Reynolds, M. A. Wyczalkowski, L. Yao, L. Yu, S. Q. Sun, G. Fusion Analysis Working, N. Cancer Genome Atlas Research, K. Chen, A. J. Lazar, R. C. Fields, M. C. Wendl, B. A. Van Tine, R. Vij, F. Chen, M. Nykter, I. Shmulevich and L. Ding (2018). "Driver Fusions and Their Implications in the Development and Treatment of Human Cancers." *Cell Rep* **23**(1): 227-238 e223. *Co-first authors contributed equally.

3. Dang, H. X., B. S. White, **S. M. Foltz**, C. A. Miller, J. Luo, R. C. Fields and C. A. Maher (2017). "ClonEvol: clonal ordering and visualization in cancer sequencing." *Ann Oncol* **28**(12): 3076-3082.

4. **Foltz, S. M.**, W. W. Liang, M. Xie and L. Ding (2017). "MIRMMR: binary classification of microsatellite instability using methylation and mutations." *Bioinformatics* **33**(23): 3799-3801.

5. Olfson, E., N. L. Saccone, E. O. Johnson, L. S. Chen, R. Culverhouse, K. Doheny, **S. M. Foltz**, L. Fox, S. M. Gogarten, S. Hartz, K. Hetrick, C. C. Laurie, B. Marosy, N. Amin, D. Arnett, R. G. Barr, T. M. Bartz, S. Bertelsen, I. B. Borecki, M. R. Brown, D. I. Chasman, C. M. van Duijn, M. F. Feitosa, E. R. Fox, N. Franceschini, O. H. Franco, M. L. Grove, X. Guo, A. Hofman, S. L. Kardia, A. C. Morrison, S. K. Musani, B. M. Psaty, D. C. Rao, A. P.

Reiner, K. Rice, P. M. Ridker, L. M. Rose, U. M. Schick, K. Schwander, A. G. Uitterlinden, D. Vojinovic, J. C. Wang, E. B. Ware, G. Wilson, J. Yao, W. Zhao, N. Breslau, D. Hatsukami, J. A. Stitzel, J. Rice, A. Goate and L. J. Bierut (2016). "Rare, low frequency and common coding variants in *CHRNA5* and their contribution to nicotine dependence in European and African Americans." *Mol Psychiatry* **21**(5): 601-607.

6. Ye, K., J. Wang, R. Jayasinghe, E. W. Lameijer, J. F. McMichael, J. Ning, M. D. McLellan, M. Xie, S. Cao, V. Yellapantula, K. L. Huang, A. Scott, **S. Foltz**, B. Niu, K. J. Johnson, M. Moed, P. E. Slagboom, F. Chen, M. C. Wendl and L. Ding (2016). "Systematic discovery of complex insertions and deletions in human cancers." *Nat Med* **22**(1): 97-104.

7. Yao, N., **S. M. Foltz**, A. Y. Odisho and D. C. Wheeler (2015). "Geographic analysis of urologist density and prostate cancer mortality in the United States." *PLoS One* **10**(6): e0131578.

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## Honors and Awards

- "Best of *Cell Reports* 2018" for co-first author publication titled "Driver Fusions and Their Implications in the Development and Treatment of Human Cancers."

- "Outstanding Mentor", recognizing one mentor working with high schoolers from St. Louis through the Washington University Young Scientist Program (25th Anniversary Gala, October 22, 2016).

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## Teaching Experience

**Washington University in St. Louis, St. Louis, MO**

*Instructor*, Introduction to Python – Bioinformatics                                        Winter 2019
Student profile: 6 post-baccalaureate students from the Opportunities in Genomics Research diversity outreach program.
Responsibilities: Developed syllabus, created course content, led weekly classroom lectures and activities, gathered regular feedback.

*Teaching assistant*, Genomics (Biol 5488)                                        Spring 2016
Student profile: 40 first-year graduate students with different academic backgrounds and a wide range of programming experience.
Responsibilities: Taught scientific and computational concepts for weekly programming labs (Python), hosted office hours, evaluated student performance on labs and exams (one of four TAs).

*Tutor*, Fundamentals of Biostatistics for Graduate Students (Biol 5075)          Fall 2015, Fall 2016
Student profile: 30 first-year graduate students mostly lacking computational experience.
Responsibilities: Taught background bioinformatics and computer coding skills (Python) for dry lab assignments.

**Presbyterian College, Clinton, SC**

*Tutor*, Department of Mathematics                                   January 2007 – April 2010
Student profile: Individuals or groups of undergraduate students from courses up to Calculus II.
Responsibilities: Re-taught underlying concepts to help students understand their homework.

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## Mentoring Experience

### Mentoring for Ding Lab rotation graduate students

- Yize Li (Fall 2017)
  Current status: joined the lab

- Ruiyang Liu (Fall 2017)
  Current status: joined the lab

- Lijun Yao (Fall 2017)
  Current status: joined the lab

### Mentoring for Ding Lab undergraduate students

- Moses Schindler (Summer – Fall 2019)
  Current status: Washington University in St. Louis, Class of 2023

- Jessika Baral (Fall 2018)
  Current status: Washington University in St. Louis, Class of 2021

- Guanlan Dong (Fall 2018, Spring 2019)
  Graduated Washington University in St. Louis: Spring 2019
  Current status: graduate student at Harvard University

- Justin Chen (Summer 2018)
  Current status: Columbia University, Class of 2022

- Edwin Qiu (Spring 2018, Fall 2018)
  Current status: Washington University in St. Louis, Class of 2020

### Mentoring for Washington University Young Scientist Program high schoolers

- Jada Reid (Fall 2014 – Spring 2018)
  Graduated Collegiate School of Medicine and Bioscience: Spring 2018
  Current status: Wesleyan University, Class of 2022

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## Presentations

### Oral presentations

- "RNA-Seq and fusion discovery pipeline for a large multiple myeloma cohort." WashU DBBS Precision Medicine Pathway Retreat. October 2017.

- "RNA and DNA methylation signatures for scoring tumor stemness." WashU DBBS Precision Medicine Pathway Retreat. September 2016.

**Poster presentations**

- "Fusion gene detection across a large cohort of multiple myeloma patients." International Myeloma Workshop. Boston, MA. September 2019.

- "Comprehensive Multi-Omics Analysis of Gene Fusions in a Large Multiple Myeloma Cohort." American Society of Hematology. San Diego, CA. December 2018.

- "Multiple Myeloma RNA-seq and Fusion Discovery Pipeline." WashU DBBS Computational and Systems Biology / Human and Statistical Genetics / Molecular Genetics and Genomics Joint Program Retreat. Potosi, MO. September 2017.

- "Genomic region and sample selection strategy for variant discovery and association analysis." Genome Informatics. Cold Spring Harbor, NY. October, 2015.

- "Comprehensive Analysis of Germline Complex Insertions and Deletions." WashU DBBS Computational and Systems Biology / Molecular Genetics and Genomics Joint Program Retreat. New Haven, MO. September, 2015.

- "Comprehensive Analysis of Germline Complex Insertions and Deletions." WashU DBBS Human and Statistical Genetics Program Retreat. St. Louis, MO. September, 2015.

- "Identity-by-descent analysis of sequence data." International Genetic Epidemiology Society. Stevenson, WA. October 2012.

## Research Skills

- Programming languages: R, Python, Bash, Unix command line (github.com/envest)

- Cancer bioinformatics tools: fusion detection, copy number detection, gene expression, clonal evolution modeling

- Analysis of large-scale sequencing data (DNA, RNA) and file formats (VCF, BAM, MAF, BED) on large Unix clusters

- Appropriate use of statistical modeling, including association testing and survival analysis

- Data presentation tools: ggplot2 (R package), Adobe Illustrator, LaTeX

- Computational project management and data analysis team leadership

- Multi-institutional collaborations, e.g. The Cancer Genome Atlas (TCGA), Clinical Proteomic Tumor Analysis Consortium (CPTAC), Multiple Myeloma Research Foundation (MMRF)

## Professional Development

- Teaching Center

- SEPAL Active Learning seminar

- Mentor training

- Early Career Workshop

- Science Communication class

## Service and Outreach

**Young Scientist Program, Washington University in St. Louis, St. Louis, MO**
*Leader of Mentoring Program Cohort*                                 Fall 2014 – Spring 2018

- Led 12 graduate students paired with high schoolers for four years

- Coordinated bi-weekly school visits and field trips

- Mentored one student (Jada Reid, Wesleyan University, Class of 2022)

**St. Louis Science Center, St. Louis, MO**
*Exhibit interpreter*                                                          Summer 2015

- Smithsonian and NHGRI sponsored exhibit Genome: Unlocking Life's Code

- Discussed the science, ethics, and societal impacts of genomics with museum patrons

## Graduate School Coursework

**Washington University in St. Louis, St. Louis, MO**                June 2014 – present
Ph.D. Biology and Biomedical Sciences (Human and Statistical Genetics) (GPA: 4.00/4.00)
Human Linkage and Association Analysis; Fundamentals of Mammalian Genetics; Computational
Statistical Genetics; Genomics; Human Genetics Journal Club; Genetics and Genomics of Disease;
Ethics and Research Science; Communicating Science: Writing for Multiple Audiences; Scholarship
of Teaching and Learning

**University of Washington, Seattle, WA**                September 2011 – August 2013
MS Biostatistics (GPA: 3.43/4.00)
Biostatistics I, II; Statistical Inference I, II; Theory of Linear Models; Statistical Genetics I; Categorical Data Analysis; Survival Data Analysis; Evolutionary Genetics; Population Genetics; Statistical
Genetics Seminar; Biostatistics Seminar

## Other Work Experience

**Across, Nairobi, Kenya**                                September 2010 – July 2011
*Institutional and Organizational Development Volunteer*
Promoted the organization and its mission (holistic transformation of South Sudan communities) to an international audience through the website and other publications. Placement coordinated through the Presbyterian Church (U.S.A.) Young Adult Volunteers program.

Last updated: October 12, 2019